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RESULT 1
US-08-252-384C-2
; Sequence 2, Application US/08252384C
; GENERAL INFORMATION:
; APPLICANT: Reactive Surfaces, Ltd.
; APPLICANT: McDaniel, Steven
; APPLICANT: Raushel, Frank M
; APPLICANT: Wild, James R
; TITLE OF INVENTION: Recombinant Organophosphorous Acid Anhydrase and Methods
of Use
; FILE REFERENCE: TAMK145
; CURRENT APPLICATION NUMBER: US/08/252,384C
; CURRENT FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: US 07/928,540
; PRIOR FILING DATE: 1992-08-13
; PRIOR APPLICATION NUMBER: US 07/344,258
; PRIOR FILING DATE: 1989-04-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Pseudomonas diminuta
US-08-252-384C-2

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Query Match          100.0%; Score 1831; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.5e-170;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     61 SSAGFLRAWPEFFGSRKALAEKAVRGLRRARAAGVRTIVDVSTFDIGRDVSLLAEVSRAA 120

Qy    121 DVHIVAATGLWFDPPPLSMRLRSVEELTQFFLREIQYGIEDTGIRAGIIKVATTGKATPPFQ 180
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Db    181 ELVLKAAARASLATGVPVTTHTAASQRDGEQQAAIFESEGLSPSRVCIGHSDDTDDLSTYL 240

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Db    361 TLRAS 365

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RESULT 8

US-08-252-384B-2

; Sequence 2, Application US/08252384B

; GENERAL INFORMATION:

; APPLICANT: Reactive Surfaces, Ltd.

; TITLE OF INVENTION: Recombinant Organophosphorus Acid Anhydrase and Methods of Use

; FILE REFERENCE: RACT-00100

; CURRENT APPLICATION NUMBER: US/08/252,384B

; CURRENT FILING DATE: 1994-06-01

; PRIOR APPLICATION NUMBER: 07/928,540

; PRIOR FILING DATE: 1992-08-13

; PRIOR APPLICATION NUMBER: 08/252,384

; PRIOR FILING DATE: 1994-06-01

; PRIOR APPLICATION NUMBER: 07/344,258

; PRIOR FILING DATE: 1989-04-27

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2

; LENGTH: 337

; TYPE: PRT

; ORGANISM: Pseudomonas diminuta

US-08-252-384B-2

Query Match 90.3%; Score 1653; DB 12; Length 337;

Best Local Similarity 99.7%; Pred. No. 3.3e-112;

Matches 327; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy	90	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF	149
Db	62	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF	121
Qy	150	FLREIQYGIEDTGIRAGIIKVAT	TGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG	209
Db	122	FLREIQYGIEDTGIRAGIIKVAT	TGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG	181
Qy	210	EQQAAIFESEGLSPSRVCIGHSD	DDTDDLSTALAAARGYLIGLDHIPHSAIGLEDNASAS	269
Db	182	EQQAAIFESEGLSPSRVCIGHSD	DDTDDLSTALAAARGYLIGLDHIPHSAIGLEDNASAS	241
Qy	270	ALLGIRSWQTRALLIKALIDQGY	MKQILVSNLWLFSSYVTNIMDVM DRVNP DGM AFIP	329
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US-08-252-384A-1

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; Sequence 1, Application US/08252384A
; GENERAL INFORMATION:
; APPLICANT: Reactive Surfaces
; APPLICANT: McDaniel, C. Steven
; TITLE OF INVENTION: Recombinant Organophosphorus Acid Anhydrase and Methods
of Use
; FILE REFERENCE: RACT-00200
; CURRENT APPLICATION NUMBER: US/08/252,384A
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: 07/928,540
; PRIOR FILING DATE: 1992-08-13
; PRIOR APPLICATION NUMBER: 08/252,384
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 07/344,258
; PRIOR FILING DATE: 1989-04-27
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-08-252-384A-1
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Best Local Similarity 100.0%; Pred. No. 3.9e-115;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      2 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 61

Qy      90 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHI VAATGLWFDPPLSMRLRSVEELTQF 149
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Db      62 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHI VAATGLWFDPPLSMRLRSVEELTQF 121

Qy     150 FLREIQYGIEDTGIRAGI IKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 209
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Db     182 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASAS 241

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Qy     330 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 365
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RESULT 2

US-08-252-384B-1

; Sequence 1, Application US/08252384B

; GENERAL INFORMATION:

; APPLICANT: Reactive Surfaces, Ltd.

; TITLE OF INVENTION: Recombinant Organophosphorus Acid Anhydrase and Methods of Use

; FILE REFERENCE: RACT-00100

; CURRENT APPLICATION NUMBER: US/08/252,384B

; CURRENT FILING DATE: 1994-06-01

; PRIOR APPLICATION NUMBER: 07/928,540

; PRIOR FILING DATE: 1992-08-13

; PRIOR APPLICATION NUMBER: 08/252,384

; PRIOR FILING DATE: 1994-06-01

; PRIOR APPLICATION NUMBER: 07/344,258

; PRIOR FILING DATE: 1989-04-27

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1

; LENGTH: 1014

; TYPE: DNA

; ORGANISM: Pseudomonas diminuta

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1011)

US-08-252-384B-1

Query Match 74.6%; Score 997.4; DB 12; Length 1014;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1009; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy      210 GGTTCACACTGACTCACGAGCACATCTGCGGCAGCTCGGCAGGATTCTTGCGTGCTTGG 269
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Qy      270 CCAGAGTTCTTCGGTAGCCGCAAAGCTCTAGCGGAAAAGGCTGTGAGAGGATTGCGCCGC 329
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Db      304 TTGTGGTTTCGACCCGCCACTTTCGATGCGATTGAGGAGTGTAGAGGAACTCACACAGTTC 363

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RESULT 2

5484728-2

;Patent No. 5484728

; APPLICANT: SEERDAR, CUNEY M.;MURDOCK, DOUGLAS

; TITLE OF INVENTION: PARATHION HYDROLASE ANALOGS AND METHODS

;FOR PRODUCTION AND PURIFICATION

; NUMBER OF SEQUENCES: 6

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/333, 8892

; FILING DATE: 01-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 898,973

; FILING DATE: 25-JUN-1992

; APPLICATION NUMBER: 312,503

; FILING DATE: 17-FEB-1989

; APPLICATION NUMBER: 237,255

; FILING DATE: 26-AUG-1988

;SEQ ID NO:2:

; LENGTH: 365

5484728-2

Query Match 99.4%; Score 1688; DB 6; Length 365;

Best Local Similarity 99.7%; Pred. No. 6.9e-174;

Matches 335; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      62 ARAAGVRTIVDVSTFDIGRDVSLAEVSRAADVHI VAATGLWFDPPLSMRLRSVEELTQF 121
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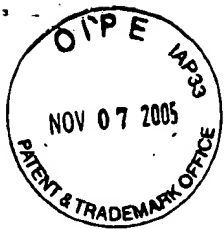
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Qy      302 LRVIPFLREKGVPQETLAGITVTNIPARFLSPTLRAS 337
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in patent #U(N)



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RACT-00100.ST25
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McDaniel, Steven
Raushel, Frank M
Wild, James R

<120> Recombinant Organophosphorous Acid Anhydrase and Methods of Use

<130> TAMK145

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<141> 1994-06-01

<150> US 07/928,540
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Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Ala Gly 15
1 5 10
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RACT-00100.ST25																
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Leu	Gly	Ile	Arg	Ser	Trp	Gln	Thr	Arg	Ala	Leu	Leu	Ile	Lys	Ala	Leu	
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RACT-00100.ST25

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35 40 45

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Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Ala Gly Val Arg
85 90 95

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Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu
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Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro Ser
210 215 220

Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr Leu
225 230 235 240

Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro
245 250 255

His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu Leu
260 265 270

Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile
275 280 285

Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe
290 295 300

Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val
305 310 315 320

Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe Leu
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SEQUENCE LISTING

- <110> Reactive Surfaces, Ltd.
- <120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use
- <130> RACT-00100
- <140> US 08/252,384 A
- <141> 2004-06-01
- <150> 07/928,540
- <151> 1992-08-13
- <150> 08/252,384
- <151> 1994-06-01
- <150> 07/344,258
- <151> 1989-04-27
- <160> 2
- <170> PatentIn version 3.3
- <210> 1
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- <212> DNA
- <213> Pseudomonas diminuta



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- <221> CDS
- <222> (1)..(1011)

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Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly
20        25        30

agc tcg gca gga ttc ttg cgt gct tgg cca gag ttc ttc ggt agc cgc      144
Ser Ser Ala Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg
35        40        45

aaa gct cta gcg gaa aag gct gtg aga gga ttg cgc cgc gcc aga gcg      192
Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala
50        55        60

gct ggc gtg cga acg att gtc gat gtg tcg act ttc gat atc ggt cgc      240
Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
65        70        75        80

gac gtc agt tta ttg gcc gag gtt tcg cgg gct gcc gac gtt cat atc      288
Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile
85        90        95

gtg gcg gcg acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg      336
Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
100       105       110

agg agt gta gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat      384
Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr

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tca gcc ctc ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile 245 250 255			768
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atc act gtg act aac ccg gcg cgg ttc tat gtc acc gac ctt gcg ggc Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly 325 330 335			1008
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Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala
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Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
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Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile
85 90 95

Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
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Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr
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Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr
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Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala
165 170 175

Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
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195 200 205

Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
210 215 220

Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
225 230 235 240

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245 250 255

Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
260 265 270

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val
275 280 285

Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val
290 295 300

Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
305 310 315 320

Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly
325 330 335

Val



Organization Applicant RACT00200 2nd Amd Seq Listing.WorkFile

Street :
City :
State :
Country :
PostalCode :
PhoneNumber :
FaxNumber :
EmailAddress :

<110> OrganizationName : Reactive Surfaces, Ltd.

Application Project

<120> Title : Recombinant Organophosphorus Acid Anhydrase and Methods of Use
<130> AppFileReference : RACT-00200
<140> CurrentAppNumber : Unknown
<141> CurrentFilingDate : 2003-01-02

Earlier Applications

<150> PriorAppNumber : 07/928,540
<151> PriorFilingDate : 1992-08-13

Earlier Applications

<150> PriorAppNumber : 08/252,384
<151> PriorFilingDate : 1994-06-01

Earlier Applications

<150> PriorAppNumber : 07/344,258
<151> PriorFilingDate : 1989-04-27

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tggccagagt tcttcggtag ccgcaaagct ctagcggaaa aggctgtgag aggattgcgc 180
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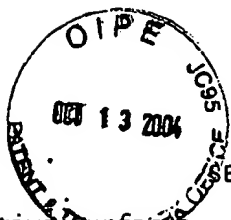
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SequenceDescription :

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- <110> Reactive Surfaces
McDaniel, C. Steven
- <120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use
- <130> RACT-00200
- <140> Unknown
- <141> 2002-12-23
- <150> 07/928,540
- <151> 1992-08-13
- <150> 08/252,384
- <151> 1994-06-01
- <150> 07/344,258
- <151> 1989-04-27
- <160> 1
- <170> PatentIn version 3.2
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- <213> Pseudomonas aeruginosa
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Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
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RACT00200 Sequence Listing

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Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
 180 185 190

Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp
 195 200 205

Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
 210 215 220

Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
 225 230 235 240

Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile
 245 250 255

Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
 260 265 270

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val
 275 280 285



Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val
 290 295 300

Ile Pro Phe Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
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SEQUENCE LISTING



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<120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use
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Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
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Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
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195 200 205

Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
210 215 220

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Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
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290 295 300

Ile Pro Phe Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
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SEQUENCE LISTING

<110> Reactive Surfaces, Ltd.

<120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use

<130> RACT-00200

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<150> 07/928,540

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70

75

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90

95

gtg gag gcg acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg
336
Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu

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105

110

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120

125

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Val

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Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala
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Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
65 70 75 80

Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile
85 90 95

Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
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Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr
115 120 125

Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr
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Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
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Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
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Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
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Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly
325 330 335

Val

Protein Comparisons Percent Identity

McDaniel vs Wild Lab 57.8%
McDaniel vs Serdar 59.5%
Serdar vs Wild Lab 100%

DNA Comparisons Percent Identity

McDaniel vs Wild Lab 88.0%
McDaniel vs Serdar 83.7%
Serdar vs Wild Lab 99.6%

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Serdar.pro Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Arg Thr Leu Leu Gly Gly Leu Ala Gly Cys Ala Thr Trp Leu Asp Arg 30

McDaniel.pro Ser Ala Gln Ala Met Arg Ser Ile Arg Ala Arg Pro Ile Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu Asp Ile Ser Ala 58
Wild Lab.PRO Ser Ala Gln Ala Met Arg Ser Ile Arg Ala Arg Pro Ile Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu Asp Ile Ser Ala 58
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McDaniel.pro Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20
Wild Lab.PRO Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20
Serdar.pro Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20

McDaniel.pro Gln Arg Asp Gly Glu Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 23
Wild Lab.PRO Gln Arg Asp Gly Glu Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 23
Serdar.pro Gln Arg Asp Gly Glu Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 23

McDaniel.pro Asp Leu Ser Tyr Leu Thr Ala Leu Leu Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn 26
Wild Lab.PRO Asp Leu Ser Tyr Leu Thr Ala Leu Leu Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn 26
Serdar.pro Asp Leu Ser Tyr Leu Thr Ala Leu Leu Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn 26

McDaniel.pro Ala Ser Ala Ser Pro Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln 29
Wild Lab.PRO Ala Ser Ala Ser Pro Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln 29
Serdar.pro Ala Ser Ala Ser Pro Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln 29

McDaniel.pro Ile Leu Val Ser Asn Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val Asn Pro Asp Gly Met 32
Wild Lab.PRO Ile Leu Val Ser Asn Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val Asn Pro Asp Gly Met 32
Serdar.pro Ile Leu Val Ser Asn Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val Asn Pro Asp Gly Met 32

McDaniel.pro Ala Phe Ile His 32
Wild Lab.PRO Ala Phe Ile His 32
Serdar.pro Ala Phe Ile His 32

McDaniel.pro Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser 32
Wild Lab.PRO Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser 32
Serdar.pro Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser 36

```

Decoration 'Decoration #1': Shade (with black at 10% fill) residues that differ from McDaniel.pro.

Decoration 'Decoration #2': Box residues that differ from McDaniel.pro.

[illegible]

Decorations 'Decorations VI': Spade (with black as 1st (11)) residues that differ from McDonald P diminuta, seq.

Decorations 'Decorations 02': Nox residues that differ from McDaniel & diminuta.ssp.

Works Cited

McDaniel P. diminuta :

McDaniel, C.S., Harper, L.L. and Wild, J.R., Cloning and sequencing of a plasmid-borne gene (opd) encoding a phosphotriesterase, J. Bacteriol. 170 (5), 2306-2311 (1988). Gene Bank Accession Number: M20392

Oph-lab RC: Wild lab DNA sequence

Serdar: Serdar Sequence obtained from United States Patent and Trademark Office (uspto.gov) Patent Number 5,484,728

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FILED 12-23-02 AND 01-02-03.

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	1693	99.7	365	2	A43720	parathion hydrolas		
2	913	53.8	325	2	A28214	phosphotriesterase		
3	448	26.4	326	2	D70962	hypothetical prote		
4	408	24.0	314	2	F90424	hypothetical prote		
5	385	22.7	323	2	E75459	probable phosphotr		
6	331	19.5	305	2	AB1321	probable phosphotr		
7	309	18.2	331	2	A83678	hypothetical prote		
8	308	18.1	292	2	F65132	hypothetical 32.9		
9	296	17.4	679	2	F83723	hypothetical prote		
10	277.5	16.3	355	2	AD2933	hypothetical prote		
11	277.5	16.3	355	2	C98349	resiniferatoxin-bi		
12	273	16.1	344	2	AC0994	puative phophotrie		
13	269.5	15.9	330	2	AG1405	Phosphotriesterase		
14	268.5	15.8	330	2	AG1781	Phosphotriesterase		
15	229	13.5	351	2	A99586	conserved hypothet		

RESULT 1

A43720

parathion hydrolase precursor - *Flavobacterium* sp. (ATCC 27551)

C;Species: *Flavobacterium* sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 08-Oct-1999

C;Accession: A43720

R;Mulbry, W.W.; Kams, J.S.

J. Bacteriol. 171, 6740-6746, 1989

A;Title: Parathion hydrolase specified by the *Flavobacterium* opd gene: relationship between the gene and protein.

A;Reference number: A43720; MUID:90078122; PMID:2556372

A;Accession: A43720

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-365 <MUL>

A;Cross-references: GB:M29593; NID:g148712; PIDN:AAA24930.1; PID:g148713

A;Experimental source: ATCC 27551

Query Match 99.7%; Score 1693; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-126;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2

SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR
61

|||||

Db 30

SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR
89

Qy 62

ARAAGVRTIVDVSTFDIGRDVSLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF
121

|||||

Db 90

ARAAGVRTIVDVSTFDIGRDVSLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF
149

Qy 122

FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG

181

|||||

Db 150

FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG

209

Qy 182

EQQAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS

241

|||||

Db 210

EQQAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS

269

Qy 242

ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP

301

|||||

Db 270

ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP

329

Qy 302 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 337

|||||

Db 330 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 365

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1695	99.8	337	5	ABB79958	Abb79958 Organopho
2	1693	99.7	336	6	ABG72651	Abg72651 Flavobact
3	1693	99.7	365	2	AAR05573	Aar05573 Parathion
4	1693	99.7	365	6	ABB82802	Abb82802 Flavobact
5	1689	99.5	336	6	ABG72650	Abg72650 Flavobact
6	1686	99.3	357	2	AAy43487	Aay43487 Amino aci
7	1685	99.2	334	2	AAy43486	Aay43486 Amino aci
8	1558	91.8	356	6	ABB82799	Abb82799 A. radiob
9	1558	91.8	384	6	ABB82798	Abb82798 A. radiob
10	1552	91.4	384	6	ABB82801	Abb82801 A. radiob
11	1535	90.4	384	6	ABB82800	Abb82800 A. radiob
12	465	27.4	326	6	ABU33918	Abu33918 Protein e
13	448	26.4	326	6	ABU36432	Abu36432 Protein e
14	400	23.6	306	6	ABU34486	Abu34486 Protein e
15	372.5	21.9	346	6	ABU31613	Abu31613 Protein e
16	331	19.5	305	5	ABB48499	Abb48499 Listeria
17	331	19.5	305	6	ABU32460	Abu32460 Protein e
18	308	18.1	292	6	ABU14978	Abu14978 Protein e
19	283	16.7	345	6	ABU21704	Abu21704 Protein e
20	273	16.1	344	6	ABU47684	Abu47684 Protein e
21	273	16.1	344	6	ABU47288	Abu47288 Protein e
22	269.5	15.9	330	5	ABB47719	

RESULT 1

ABB79958

ID ABB79958 standard; protein; 337 AA.

XX

AC ABB79958;

XX

DT 12-DEC-2002 (first entry)

XX

DE Organophosphorous hydrolase.

XX

KW Organophosphorous hydrolase; OPH; enzyme; immobilisation;

KW chemical warfare; pesticide; pollutant; detoxification; decontamination.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Peptide 1. .29

FT /label= Signal_peptide

FT Protein 30. .337

FT /label= Mature_protein

XX

PN WO200268454-A2.

XX

PD 06-SEP-2002.

XX

PF 21-FEB-2002; 2002WO-US005755.

XX

PR 21-FEB-2001; 2001US-00791138.

PR 20-FEB-2002; 2002US-00081737.

XX

PA (BATT) BATTELLE MEMORIAL INST.

XX

PI Ackerman EJ, Liu J, Chenghong L;

XX

DR WPI; 2002-713364/77.

DR N-PSDB; ABQ81428.

XX

PT Protein system, for facilitating chemical reactions e.g. hydrolysis,

PT oxidation, hydrogenation and proteolysis, comprises porous matrix

PT material and protein within matrix.

XX

PS Example; Fig 4; 56pp; English.

XX

CC The present sequence is the protein sequence of an organophosphorous
 CC hydrolase (OPH) encoded by an expression plasmid of the invention. The
 CC invention provides a method for producing OPH by transfecting a host cell
 CC with a vector comprising a sequence encoding OPH linked to a T7
 CC expression control sequence, culturing the transfected host cell, and
 CC purifying OPH from the cell or culture medium. This OPH has an activity
 CC of about 13,000 U/mg. The host cell can be prokaryotic, e.g. Escherichia
 CC coli, or eukaryotic, e.g. Pichia pastoris. The invention also provides a
 CC protein system for facilitating chemical reactions. The protein system
 CC comprises a porous matrix material having a pore volume of which at least
 CC 90% is composed of pores of 50-400 Angstroms. The protein occupies 5-40%
 CC of the average pore volume, and is preferably an enzyme, especially OPH
 CC having an activity of 60-95% that of the active state and retaining about
 CC 10% of its activity after 24 hr under alkaline conditions. The porous

CC matrix may comprise surface hydroxyls that are reacted with a coupling
CC agent to form a functionalised monolayer. The system provides high enzyme
CC activities on a porous support, stability under a variety of conditions,
CC high densities of active protein and capability in industrial-scale
CC applications. It provides environmentally safe methods of destroying
CC chemical weapons and organophosphorous pesticides while avoiding the
CC dangers inherent in burning these materials. It can be used in filtration
CC equipment for individual soldiers and pesticide workers, and in vehicles,
CC aircraft, ships and buildings such as civilian and military defence
CC shelters, to perform detoxifications

XX

SQ Sequence 337 AA;

Query Match 99.8%; Score 1695; DB 5; Length 337;
Best Local Similarity 99.7%; Pred. No. 1.1e-163;
Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MSIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLR 60
          |||
Db      1 MSIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLR 60

Qy     61 RARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHI VAATGLWFDPPPLSMRLRSVEELTQ 120
          |||
Db     61 RARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHI VAATGLWFDPPPLSMRLRSVEELTQ 120

Qy    121 FFLREIQYGI EDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRD 180
          |||
Db    121 FFLREIQYGI EDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRD 180

Qy    181 GEQQA AIFESEGLSPSRVCIGHSDDTDDL SYLTALAARGYLIGLDH I PHSAIGLEDNASA 240
          |||
Db    181 GEQQA AIFESEGLSPSRVCIGHSDDTDDL SYLTALAARGYLIGLDH I PHSAIGLEDNASA 240

Qy    241 SALLGIRSWQTRALLIKALIDQGYMKQILVSN DWLFGFSSYVTNIMDVMDRVNPDGMAFI 300
          |||
Db    241 SALLGIRSWQTRALLIKALIDQGYMKQILVSN DWLFGFSSYVTNIMDVMDRVNPDGMAFI 300

Qy    301 PLRVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 337
          |||
Db    301 PLRVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 337
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Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	1688	99.4	365	2	Q8GC45	Q8gc45	flavobacter
2	1630	96.0	365	2	Q8VLR0	Q8vlr0	chryseobact
3	1558	91.8	384	2	Q93LD7	Q93ld7	agrobacteri
4	915	53.9	325	2	Q47934	Q47934	flavobacter
5	448	26.4	326	16	Q7U2I4	Q7u2i4	mycobacteri
6	408	24.0	314	17	Q97VT7	Q97vt7	sulfolobus
7	385	22.7	323	16	Q9RVU2	Q9rvu2	deinococcus
8	331	19.5	305	16	Q8Y5T5	Q8y5t5	listeria mo
9	325.5	19.2	362	16	Q985I1	Q985i1	rhizobium l
10	309	18.2	331	16	Q9KG87	Q9kg87	bacillus ha
11	306	18.0	292	16	Q8FCW5	Q8fcw5	escherichia
12	304	17.9	292	16	Q7UAS1	Q7uas1	shigella fl
13	296	17.4	679	16	Q9KF95	Q9kf95	bacillus ha
14	288	17.0	344	16	Q8FG90	Q8fg90	escherichia
15	277.5	16.3	355	16	Q8UBF0	Q8ubf0	agrobacteri
16	273	16.1	344	16	Q8XFU6	Q8xfu6	salmonella
17	270.5	15.9	349	13	Q7SZS2	Q7szs2	xenopus lae
18	269.5	15.9	330	16	Q8Y427	Q8y427	listeria mo
19	268.5	15.8	330	16	Q927J1	Q927j1	listeria in

08GC45

Query Match 99.4%; Score 1688; DB 2; Length 365;
Best Local Similarity 99.7%; Pred. No. 8.6e-124;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	61
Db	30	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	89
Qy	62	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHI VAATGLWFDPP	121
Db	90	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHI VAATGLWFDPP	149
Qy	122	FLREIQYGI EDTGIRAGI I	KVATTGKATPFQELVLKAAARAS	181
Db	150	FLREIQYGI EDTGIRAGI I	KVATTGKAAPFQELVLKAAARAS	209
Qy	182	EQQAAIFESEGLSPSRVCIGH	SDDTDDL SYLTALAARGYLIGL	241
Db	210	EQQAAIFESEGLSPSRVCIGH	SDDTDDL SYLTALAARGYLIGL	269

```

Qy      242 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFQFSSYVTNIMDVMDRVNPDGMAFIP 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      270 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFQFSSYVTNIMDVMDRVNPDGMAFIP 329

Qy      302 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 337
          ||||||||||||||||||||||||||||||||||||
Db      330 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 365

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RESULT 2

Q8VLR0

ID Q8VLR0 PRELIMINARY; PRT; 365 AA.
 AC Q8VLR0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Parathion hydrolase precursor (EC 3.1.8.1).
 GN OPD.
 OS Chryseobacterium balustinum.
 OG Plasmid pBC9.
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
 OC Flavobacteriaceae; Chryseobacterium.
 OX NCBI_TaxID=246;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Siddavatam D., Manavathi B., Merrick M.;
 RT "The conserved region surrounding the organophosphorus pesticide
 RT degrading (opd) gene on the Flavobacterium plasmid pPDL2 has the
 RT features of a complex transposon.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ426431; CAD19996.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0004063; F:aryldialkylphosphatase activity; IEA.
 DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009056; P:catabolism; IEA.
 DR InterPro; IPR001559; PTE.
 DR Pfam; PF02126; PTE; 1.
 DR PROSITE; PS01322; PHOSPHOTRIESTERASE_1; 1.
 DR PROSITE; PS01323; PHOSPHOTRIESTERASE_2; 1.
 KW Signal; Hydrolase; Plasmid.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 365 PARATHION HYDROLASE.
 SQ SEQUENCE 365 AA; 39116 MW; AA9EC0E3BDD3F811 CRC64;

Query Match 96.0%; Score 1630; DB 2; Length 365;
 Best Local Similarity 96.4%; Pred. No. 3e-119;
 Matches 324; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 61
 |||
 Db 30 SIGTGDRINTVRGPITNSEAGFTLTHEHICGTSAGFLRAWQEFFGSRKALAEKAVRGLRR 89
 Qy 62 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHIVAATGLWFDPPPLSMRLRSVEELTQF 121
 ||| :|
 Db 90 ARAAGVRTIVDVSTFDIGRDVSLLAEVSMMDVSLLAETGLWFDPPPLSIGLRSVEELTQF 149
 Qy 122 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 181
 |||
 Db 150 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 209
 Qy 182 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASAS 241
 |||
 Db 210 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASAS 269
 Qy 242 ALLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFIP 301

Db 270 |||||ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 329

Qy 302 LRVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 337

Db 330 |||||LRVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 365

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1689	99.5	336	4	US-09-603-450-4	Sequence 4, Appli
2	1688	99.4	365	6	5484728-2	Patent No. 5484728
3	267	15.7	352	4	US-09-543-681A-8100	Sequence 8100, Ap
4	238.5	14.0	349	1	US-08-343-027A-12	Sequence 12, Appl
5	105	6.2	477	4	US-09-489-039A-9937	Sequence 9937, Ap
6	104	6.1	495	4	US-09-252-991A-21509	Sequence 21509, A
7	99.5	5.9	2482	4	US-09-252-991A-16967	Sequence 16967, A
8	92	5.4	908	4	US-09-328-352-7168	Sequence 7168, Ap
9	91.5	5.4	461	4	US-09-134-000C-5551	Sequence 5551, Ap
10	90.5	5.3	647	4	US-09-725-735A-18	Sequence 18, Appl
11	90	5.3	569	4	US-09-543-681A-5106	Sequence 5106, Ap
12	89.5	5.3	1161	4	US-09-252-991A-22872	Sequence 22872, A
13	89	5.2	403	4	US-09-252-991A-25706	Sequence 25706, A
14	89	5.2	655	4	US-09-107-532A-4425	Sequence 4425, Ap
15	88.5	5.2	283	4	US-09-543-681A-8240	Sequence 8240, Ap
16	87	5.1	288	4	US-09-252-991A-18721	Sequence 18721, A
17	87	5.1	476	4	US-09-489-039A-14013	Sequence 14013, A

RESULT 1

US-09-603-450-4

; Sequence 4, Application US/09603450

; Patent No. 6469145

; GENERAL INFORMATION:

; APPLICANT: Rastogi, Vipin K

; APPLICANT: Cheng, Tu-c

; APPLICANT: DeFrank, Joseph J

; TITLE OF INVENTION: One-Step Purification Process for Organophosphorus

; TITLE OF INVENTION: Hydrolase Enzyme

; FILE REFERENCE: DAM-508-99

; CURRENT APPLICATION NUMBER: US/09/603,450

; CURRENT FILING DATE: 2000-06-26

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 336

; TYPE: PRT

; ORGANISM: Flavobacterium sp

US-09-603-450-4

Query Match 99.5%; Score 1689; DB 4; Length 336;

Best Local Similarity 100.0%; Pred. No. 4.7e-174;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3  IGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRA 62
          |||
Db      2  IGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRA 61

Qy     63  RAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHI VAATGLWFDPPLSMRLRSVEELTQFF 122
          |||
Db     62  RAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHI VAATGLWFDPPLSMRLRSVEELTQFF 121

Qy    123  LREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGE 182
          |||
Db    122  LREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGE 181

Qy    183  QQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASASA 242
          |||
Db    182  QQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASASA 241

Qy    243  LLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFIPL 302
          |||
Db    242  LLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFIPL 301

Qy    303  RVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 337
          |||
Db    302  RVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 336

```

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	1693	99.7	365	1	OPD_FLASP	P16648 flavobacter
2	448	26.4	326	1	PHP_MYCTU	P96413 mycobacteri
3	308	18.1	292	1	PHP_ECOLI	P45548 escherichia
4	243.5	14.3	349	1	PTER_HUMAN	Q96bw5 homo sapien
5	242.5	14.3	349	1	PTER_RAT	Q63530 rattus norv
6	239.5	14.1	349	1	PTER_MOUSE	Q60866 mus musculu
7	211.5	12.5	350	1	PTER_DROME	Q9vhf2 drosophila
8	127	7.5	216	1	YE97_MYCPN	P75290 mycoplasma
9	103	6.1	226	1	GPH2_PSEAE	Q9hz62 pseudomonas
10	103	6.1	319	1	HE31_STRCO	Q9wx16 streptomyce
11	96	5.7	342	1	ARGC_STRCO	P54895 streptomyce
12	93.5	5.5	352	1	TFTE_BURCE	Q45072 burkholderi
13	93	5.5	3421	1	TEGU_HSVEB	P28955 equine herp
14	92.5	5.4	522	1	LEU1_DEIRA	Q9rua9 deinococcus
15	92.5	5.4	898	1	SYA_METTH	O27718 methanobact
16	92	5.4	486	1	LE11_PYRAB	Q9uz08 pyrococcus
17	92	5.4	617	1	VATA_MANSE	P31400 manduca sex
18	91.5	5.4	494	1	TYRO_RHIME	P33180 rhizobium m
19	91.5	5.4	520	1	LEU1_YERPE	Q8zig8 yersinia pe
20	91.5	5.4	1139	1	VRNA_BSMV	P17595 barley stri
21	91	5.4	1290	1	RPOC_MYCPN	P75271 mycoplasma
22	90.5	5.3	333	1	YF72_HALN1	Q9hpl8 halobacteri
23	90.5	5.3	838	1	GLGB_STRAW	Q82jf0 streptomyce
24	89.5	5.3	300	1	Y505_MYCLE	Q49823 mycobacteri
25	89.5	5.3	308	1	Y505_MYCTU	Q11169 mycobacteri
26	89.5	5.3	435	1	PROA_BRAJA	Q89x85 bradyrhizob
27	89.5	5.3	958	1	GCP2_PSEAE	Q9htx7 pseudomonas
28	89	5.2	614	1	VAA2_DROME	Q27331 drosophila

RESULT 1

OPD_FLASP

ID OPD_FLASP STANDARD; PRT; 365 AA.
AC P16648; P13739;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Parathion hydrolase precursor (EC 3.1.8.1) (Phosphotriesterase)
DE (PTE).
GN OPD.
OS Flavobacterium sp. (strain ATCC 27551), and
OS Brevundimonas diminuta (Pseudomonas diminuta).
OG Plasmid pCMS1.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Flavobacterium.
OX NCBI_TaxID=239, 293;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-53.
RC SPECIES=Flavobacterium sp ATCC 27551;
RX MEDLINE=90078122; PubMed=2556372;
RA Mulbry W.W., Karns J.S.;
RT "Parathion hydrolase specified by the Flavobacterium opd gene:
RT relationship between the gene and protein.";
RL J. Bacteriol. 171:6740-6746(1989).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-44.
RC SPECIES=B.diminuta; STRAIN=MG;
RA Serdar C.M., Murdock D.C., Rohde M.F.;
RT "Parathion hydrolase gene from Pseudomonas diminuta MG: subcloning,
RT complete nucleotide sequence, and expression of the mature portion of
RT the enzyme in Escherichia coli.";
RL Biotechnology 7:1151-1155(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.diminuta; STRAIN=MG;
RX MEDLINE=88198028; PubMed=2834339;
RA McDaniel C.S., Harper L.L., Wild J.R.;
RT "Cloning and sequencing of a plasmid-borne gene (opd) encoding a
RT phosphotriesterase.";
RL J. Bacteriol. 170:2306-2311(1988).
RN [4]
RP ACTIVE SITE.
RX MEDLINE=94206935; PubMed=8155644;
RA Kuo J.M., Raushel F.M.;
RT "Identification of the histidine ligands to the binuclear metal
RT center of phosphotriesterase by site-directed mutagenesis.";
RL Biochemistry 33:4265-4272(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES=B.diminuta;
RX MEDLINE=95092756; PubMed=7999757;
RA Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;
RT "Three-dimensional structure of phosphotriesterase: an enzyme capable
RT of detoxifying organophosphate nerve agents.";
RL Biochemistry 33:15001-15007(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC SPECIES=B.diminuta;
 RX MEDLINE=95315185; PubMed=7794910;
 RA Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;
 RT "Three-dimensional structure of the binuclear metal center of
 RT phosphotriesterase.";
 RL Biochemistry 34:7973-7978(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC SPECIES=B.diminuta;
 RX MEDLINE=96214508; PubMed=8634243;
 RA Vanhooke J.L., Benning M.M., Raushel F.M., Holden H.M.;
 RT "Three-dimensional structure of the zinc-containing
 RT phosphotriesterase with the bound substrate analog diethyl
 RT 4-methylbenzylphosphonate.";
 RL Biochemistry 35:6020-6025(1996).
 CC -!- FUNCTION: Has an unusual substrate specificity for synthetic
 CC organophosphate triesters and phosphorofluoridates. All of the
 CC phosphate triesters found to be substrates are synthetic
 CC compounds. The identity of any naturally occurring substrate for
 CC the enzyme is unknown. Has no detectable activity with phosphate
 CC monoesters or diesters and no activity as an esterase or protease.
 CC It catalyzes the hydrolysis of the insecticide paraoxon at a rate
 CC approaching the diffusion limit and thus appears to be optimally
 CC evolved for utilizing this synthetic substrate.
 CC -!- CATALYTIC ACTIVITY: Aryl dialkyl phosphate + H(2)O = dialkyl
 CC phosphate + an aryl alcohol.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit.
 CC -!- PATHWAY: Pesticide detoxification.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- BIOTECHNOLOGY: Has attracted interest because of its potential use
 CC in the detoxification of chemical waste and warfare agents and its
 CC ability to degrade agricultural pesticides such as parathion.
 CC -!- SIMILARITY: Belongs to the phosphotriesterase family.
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to multiple
 CC sequencing errors.
 CC -----
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 CC -----
 DR EMBL; M29593; AAA24930.1; -.
 DR EMBL; M20392; AAA98299.1; ALT_FRAME.
 DR PIR; A28214; A28214.
 DR PIR; A43720; A43720.
 DR PDB; 1DPM; 20-AUG-97.
 DR PDB; 1EYW; 20-DEC-00.
 DR PDB; 1EZ2; 20-DEC-00.
 DR PDB; 1HZY; 04-APR-01.
 DR PDB; 1IOB; 04-APR-01.
 DR PDB; 1IOD; 04-APR-01.
 DR PDB; 1JGM; 04-JUL-01.
 DR PDB; 1PSC; 01-APR-97.

DR PDB; 1PTA; 01-DEC-95.
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR InterPro; IPR001559; PTE.
 DR Pfam; PF02126; PTE; 1.
 DR PROSITE; PS01322; PHOSPHOTRIESTERASE_1; 1.
 DR PROSITE; PS01323; PHOSPHOTRIESTERASE_2; 1.
 KW Hydrolase; Membrane; Plasmid; Signal; Metal-binding; Zinc;
 KW 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 365 PARATHION HYDROLASE.
 FT METAL 55 55 ZINC 1.
 FT METAL 57 57 ZINC 1.
 FT METAL 169 169 ZINC 1 AND 2.
 FT METAL 201 201 ZINC 2.
 FT METAL 230 230 ZINC 2.
 FT METAL 301 301 ZINC 1.
 FT STRAND 36 39
 FT TURN 40 41
 FT STRAND 42 45
 FT HELIX 46 49
 FT STRAND 51 56
 FT STRAND 59 60
 FT TURN 63 64
 FT HELIX 65 68
 FT HELIX 70 73
 FT HELIX 76 92
 FT TURN 93 94
 FT STRAND 95 100
 FT HELIX 104 106
 FT TURN 107 107
 FT HELIX 110 120
 FT TURN 121 121
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 FT HELIX 223 225
 FT STRAND 226 228
 FT HELIX 231 233
 FT HELIX 237 246
 FT TURN 247 247
 FT STRAND 249 252
 FT TURN 255 256
 FT TURN 260 261
 FT TURN 263 264

FT	HELIX	266	272
FT	HELIX	277	289
FT	TURN	290	291
FT	HELIX	293	295
FT	STRAND	296	298
FT	STRAND	305	306
FT	TURN	311	312
FT	HELIX	313	320
FT	TURN	322	323
FT	HELIX	324	326
FT	HELIX	327	330
FT	TURN	331	331
FT	HELIX	332	338
FT	TURN	339	340
FT	HELIX	343	350
FT	TURN	351	351
FT	HELIX	352	358
SQ	SEQUENCE	365 AA;	39003 MW; 41FF8E4B029B46DC CRC64;

Query Match 99.7%; Score 1693; DB 1; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4.1e-128;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	61
Db	30	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	89
Qy	62	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF	121
Db	90	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF	149
Qy	122	FLREIQYGIEDTGIRAGIIKVATTG	KATPFQELVLKAAARASLATGVPVTTHTAASQRDG	181
Db	150	FLREIQYGIEDTGIRAGIIKVATTG	KATPFQELVLKAAARASLATGVPVTTHTAASQRDG	209
Qy	182	EQQAAlFESEGLSPSRVCIGHSD	DDTDDLSTALAAARGYLIGLDHlPHSAIGLEDNASAS	241
Db	210	EQQAAlFESEGLSPSRVCIGHSD	DDTDDLSTALAAARGYLIGLDHlPHSAIGLEDNASAS	269
Qy	242	ALLGIRSWQTRALLIKALIDQGYM	QILVSNLWLFSGSSVVTNlMDVMDRVNPDGMAFIP	301
Db	270	ALLGIRSWQTRALLIKALIDQGYM	QILVSNLWLFSGSSVVTNlMDVMDRVNPDGMAFIP	329
Qy	302	LRVIPFLREKGVPOETLAGITVTN	PARFLSPTLRAS	337
Db	330	LRVIPFLREKGVPOETLAGITVTN	PARFLSPTLRAS	365